

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Insel, Paul A.
Herrmann, Volker
Buescher, Rainer
- (ii) TITLE OF THE INVENTION: METHODS AND COMPOSITIONS FOR
IDENTIFYING GENETIC VARIATIONS IN HUMAN alpha-1B AND
beta-2-ADRENERGIC RECEPTORS
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: PALO ALTO
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Dylan, Tyler M
(B) REGISTRATION NUMBER: 37,612
(C) REFERENCE/DOCKET NUMBER: 22000-20589.00
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGGGGAAGC AAAGTTTCA

19

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGCAGTACA TGACTAGAAT

20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTCCTTGG GTGGAAGGA

19

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCTCATCAG TAAACCCAAG

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATGAGGCT TCCAGGCGTC

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATGATGCCT AACGTCTTG

19

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTCTACGTGC CCCTGGTG

18

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCCTCTAGGA CTAAGCTC

19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCGAGGAAT	TCTCTTTCCC	TCTTTTAGGT	GCTGGACAAG	TTGCATATCC	CGTTAAATCC	60
GGGGCCCCACT	CCGACAGCCC	CCTATTAAAG	GTAAGCAGCC	CCCAACCCAC	CTTTGACACG	120
GAAGAGTGAC	TAGCGGGGAA	AATAACCCCA	GCGGCCGCCT	AGGGGTGGGT	GACCCGCGAT	180
CTCCACGCCC	AGGTCCCGCC	CTCCCGCCCC	TTCCCCCGTC	CCCCCCCCCC	GTAGAGGTGA	240
CCCTGGGAGC	GGCGGGGGAG	GTTGGCTTTC	GGTCTTGCGG	GTGGTGACCC	GCGATCTCCA	300
CGCCCAAGGT	CCGCCCTCGC	GGCCCCCTGCC	CCCGCCCCCC	CCCGCAAGAG	GCGCGCCCTG	360
GGAGCGGCGG	GGTAACGCGG	CTGGCTTCCC	GGCTTGCGGG	GTGGCGGCGT	CGGGGCTGCG	420
GGCGTCCTTG	GCTGGACCCG	CATTGCCCCC	TAGTGCCGCG	CGGAGTCAGG	GCGCCGGGCT	480
CCCCCGCCTG	ATGTCACCGC	CGTGCAGTCA	GCCCAGAAGC	GGCTCATTGA	AGCAGACCCT	540

002244 1200

CTTCGGCGCT	CGCTGGGCGG	AGGAGCCGCC	GCGGTCCGCA	GACCCGAGCG	AGCTGGGCAC	600
CGCCGGGCGC	CCCCGCCTCC	CCCCCCTCCT	CCCCTCCGCT	CCCCCGCGAG	CCCGGCCAGG	660
CGCGCTCCTG	ACGTGGACCA	TTAAACTTGG	AGCTGCCGCC	TCGTCCCCCTC	TCCTCCTCCT	720
CCTCCCTCTG	ACAGGCGAGC	GAGCGACTCG	GTGCAGGCAG	GAGACGTGCT	GCGGGCTGGG	780
CTGCCCCGGG	GAGATGACTC	CTGCCAGGAG	GGGCGCCTCT	GGGAAGAAGA	CCACGGGGGA	840
AGCAAAGTTT	CAGGGCAGCT	GAGGAGCCTT	CGCCGCAGCC	CTTCCGAGCC	CAATCATCCC	900
CCTGGCTATG	GAGGGCGGAC	TCTAAGATGA	ATCCCGACCT	GGACACCGGC	CACAACACAT	960
CAGCACCTGC	CCACTGGGGA	GAGTTGAAAA	ATGCCAACTT	CACTGGCCCC	AACCAGACCT	1020
CGAGGGGGGG	CACACTGCCC	CAGCTGGACA	TCACCAGGGC	CATCTCTGTG	GGCCTGGTGC	1080
TGGGCGCCTT	CATCCTCTTT	GCCATCGTGG	GCAACATCCT	AGTCATCTTG	TCTGTGGCCT	1140
GCAACCGGCA	CCTGCGGACG	CCCACCAACT	ACTTCATTGT	CAACCTGGCC	ATGGCCGACC	1200
TGCTGTTGAG	CTTCACCGTC	CTGCCCCTCG	CAGCGGCCCT	AGAGGTGCTC	GGCTACTGGG	1260
TGCTGGGGCG	GATCTTCTGT	GACATCTGGG	CAGCCGTGGA	TGTCCTGTGC	TGCACAGCGT	1320
CCATTCTGAG	CCTGTGCGCC	ATCTCCATCG	ATCGCTACAT	CGGGGTGCGC	TACTCTCTGC	1380
AGTATCCAC	GCTGGTCACC	CGGAGGAAGG	CCATCTTGGC	GCTGCTCAGT	GTCGGGTCT	1440
TGTCCACCGT	CATCTCCATC	GGGCCTCTCC	TTGGGTGGAA	GGAGCCGGCA	CCCAACGATG	1500
ACAAGGAGTG	CGGGGTCACC	GAAGAACCCT	TCTATGCCCT	CTTCTCCTCT	CTGGGTCCTT	1560
TCTACATCCC	TCTGGCGGTC	ATTCTAGTCA	TGTACTGCCG	TGTCTATATA	GTGGCCAAGA	1620
GAACCACCAA	GAACCTAGAG	GCAGGAGTCA	TGAAGGAGAT	GTCCAACCTC	AAGGAGCTGA	1680
CCCTGAGGAT	CCATTCCAAG	AACTTTCACG	GTCCAACCTC	AAGGAGCTGA	CCCTGAGGAT	1740
CCATTCCAAG	AACTTTCACG	AGGACACCCT	TAGCAGTACC	AAGGCCAAGG	GCCACAACCC	1800
CAGGAGTTCC	ATAGCTGTCA	AACTTTTTTAA	GTTCTCCAGG	GAAAAGAAAG	CAGCTAAGAC	1860
GTTGGGCATT	GTGGTCGGTA	TGTTTCATCTT	GTGCTGGCTA	CCCTTCTTCA	TCGCTCTACC	1920
GCTTGGTAAG	TTGGGCACTA	GCAGCAGGGG	GACTGGGCAT	TTTTGGACCT	TGGGTTTACT	1980
GATGAGCTTA	CTCTAAAGTT	TTTTGTGGGT	TTTGTCTTCT	ATGCAGTCTG	TGCGTGTTCG	2040
GAGATTGAAT	AATATTGTTT	GTTCTGCAAA	GGGTTTGCAG	ATTGGGGAGC	TGGCTAAAAA	2100
CCAATCAGG	TGTTAGTAGA	ACACGCTAAG	GCACTAGCTT	CTGAAATAGA	ACCAGGGAAG	2160
GAAAATCTGG	TATGAGGAAT	GACTCACTCA	ACAGCCTCGG	TTTAATAATT	AAAAAGATAT	2220
TCACTGGGCT	TGAATATCAC	ACCGGCGTTA	TTTCAGTAGT	AATGATGTGT	CGGCTAAGGC	2280
AGCGTCACTA	ATGCAGCATA	CAAAATAGTT	TGTAGTTACT	GCAGAGACAG	CATTTGGGAA	2340
GCAGGGAGGC	AGCTCGTACA	CAGAAAGGCA	GCATTCAATC	AGCATTTCCA	GGGCTAGAGC	2400
AGAAGCCACG	CTTCTTCAAG	AGCTTTCAGA	GGCTGCATTC	TCTCCCTCCC	CTCTTCACTG	2460
ACAGCTATCA	CCCAGATATA	CTACGTTCAAT	TATCCGTTAA	TAAGAGCATT	TTACAGCCAC	2520
ACAGCCCCAA	CCAGCCTTTA	AGTTATTGAA	ATCTTGAGAT	GTGAAAGAGA	AGATGACTAG	2580
AGGGTCACAC	ATTTTTAGTT	TTTACCCCAA	AAATGTTTCT	AACTCTAGTG	ATTTATGGAA	2640
TGCCCAGAAT	CAAATTATAG	TTGTCCCTCA	TCTCAGCTGA	CAGAGACCAA	ATCCTGGTAA	2700
GATGGAATTC	GGGTACCC					2719

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCATGC	CGCGTTTCTG	TGTTGGACAG	GGGTGACTTT	GTGCCGGATG	GCTTCTGTGT	60
GAGAGCGCGC	GCGAGTGTGC	ATGTCGGTGA	GCTGGGAGGG	TGTGTCTCAG	TGTCTATGGC	120
TGTGGTTTCG	TATAAGTCTA	AGCATGTCTG	CCAGGGTGTA	TTTGTGCGCTG	TATGTGCGTG	180
CCTCGGTGGG	CACTCTCGTT	TCCTTCCGAA	TGTGGGGCAG	TGCCGGTGTG	CTGCCCTCTG	240
CCTTGAGACC	TCAAGCCGCG	CAGGCGCCCA	GGGCAGGCAG	GTAGCGGCCA	CAGAAGAGCC	300
AAAAGCTCCC	GGGTTGGCTG	GTAAGCACAC	CACCTCCAGC	TTTAGCCCTC	TGGGGCCAGC	360

CAGGGTAGCC	GGGAAGCACT	GGTGGCCCGC	CCTCCAGGGA	GCAGTTGGGC	CCCGCCCGGG	420
CCAGCCTCAG	GAGAAGGAGG	GCGAGGGGAG	GGGAGGGAAA	GGGGAGGAGT	GCCTCGCCCC	480
TTCGCGGCTG	CCGGCGTGCC	ATTGGCCGAA	AGTTCCCGTA	CGTCACGGCG	AGGGCAGTTC	540
CCCTAAAGTC	CTGTGCACAT	AACGGGCAGA	ACGCACTGCG	AAGCGGCTTC	TTCAGAGCAC	600
GGGCTGGAAC	TGGCAGGCAC	CGCGAGCCCC	TAGTACCCGA	CAAGCTGAGT	GTGCAGGACG	660
AGTCCCCACC	ACACCCACAC	CACAGCCGCT	AAATGAGGCT	TCCAGGCGTC	CGCTCGCGGC	720
CCGCAGAGCC	CCGCCGTGGG	TCCGCCTGCT	GAGGCGCCCC	CAGCCAGTGC	GCTTACCTGC	780
CAGACTGCGT	GCCATGGGGC	AACCCGGGAA	CGGCAGCGCC	TTCTTGCTGG	CACCCAATAG	840
AAGCCATGCG	CCGGACCACG	ACGTACACGA	GCAAAGGGAC	GAGGTGTGGG	TGGTGGGCAT	900
GGGCATCGTC	ATGTCTCTCA	TCGTCTTGCC	CATCGTGTTT	GGCAATGTGC	TGGTCATCAC	960
AGCCATTGCC	AAGTTCGAGC	GTCTGCAGAC	GGTCACCAAC	TACTTCATCA	CTTCACTGGC	1020
CTGTGCTGAT	CTGGTCATGG	GCCTGGCAGT	GGTGCCCTTT	GGGGCCGCCC	ATATTCTTAT	1080
GAAAATGTGG	ACTTTTGCCA	ACTTCTGGTG	GCAGTTTTTG	ACTTCCATTG	ATGTGCTGTG	1140
CGTCACGGCC	AGCATTGAGA	CCCTGTGCGT	GATCGCAGTG	GATCGCTACT	TTGCCATTAC	1200
TTCACCTTTC	AAGTACCAGA	GCCTGCTGAC	CAAGAATAAG	GCCCGGGTGA	TCATTCTGAT	1260
GGTGTGGATT	GTGTCAAGCC	TTACCTCCTT	CTTGCCCAT	CAGATGCACT	GGTACCGGGC	1320
CACCCACCAG	GAAGCCATCA	ACTGCTATGC	CAATGAGACC	TGCTGTGACT	TCTTCACGAA	1380
CCAAGCCTAT	GCCATTGCCT	CTTCCATCGT	GTCCCTTCTAC	GTTCCCTTGG	TGATCATGGT	1440
CTTCGTCTAC	TCCAGGGTCT	TTCAGGAGGC	CAAAAGGCAG	CTCCAGAAGA	TTGACAAATC	1500
TGAGGGCCGC	TTCCATGTCC	AGAACCTTAG	CCAGGTGGAG	CAGGATGGGC	GGACGGGGCA	1560
TGGACTCCGC	AGATCTTCCA	AGTTCTGCTT	GAAGGAGCAC	AAAGCCCTCA	AGACGTTAGG	1620
CATCATCATG	GGCACTTTCA	CCCTCTGCTG	GCTGCCCTTC	TTCATCGTTA	ACATTGTGCA	1680
TGTGATCCAG	GATAACCTCA	TCCGTAAGGA	AGTTTACATC	CTCCTAAATT	GGATAGGCTA	1740
TGTCAATTCT	GGTTTCAATC	CCCTTATCTA	CTGCCGGAGC	CCAGATTTCA	GGATTGCCTT	1800
CCAGGAGCTT	CTGTGCCTGC	GCAGGTCTTC	TTTGAAGGCC	TATGGGAATG	GCTACTCCAG	1860
CAACGGCAAC	ACAGGGGAGC	AGAGTGATA	TCACGTGGAA	CAGGAGAAAG	AAAATAAACT	1920
GCTGTGTGAA	GACCTCCAG	GCACGGAAGA	CTTTGTGGGC	CATCAAGGTA	CTGTGCCTAG	1980
CGATAACATT	GATTACAAG	GGAGGAATTG	TAGTACAAAT	GACTCACTGC	TGTAAAGCAG	2040
TTTTTCTACT	TTTAAAGACC	CCCCCCCCCA	ACAGAACACT	AAACAGACTA	TTTAACTTGA	2100
GGGTAATAAA	CTTAGAATAA	AATTGTAAAA	TTGTATAGAG	ATATGCAGAA	GGAAGGGCAT	2160
CCTTCTGCCT	TTTTTATTTT	TTTAAGCTGT	AAAAAGAGAG	AAAACCTATT	TGAGTGATTA	2220
TTTGTTATTT	GTACAGTTCA	GTTCTCTTTT	GCATGGAATT	TGTAAGTTTA	TGTCTAAAGA	2280
GCTTTAGTCC	TAGAGGACCT					2300